

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 17, 2004, 21:02:23 ; Search time 13.0543 Seconds

(without alignments)
4951.677 Million cell updates/sec

Title: US-08-628-829-2

Perfect score: 3467

Sequence: 1 MTAVAVAVPSKLVMTLNAGS.....PQDRPPSRRLKHPVFTTW 672

ing table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3467	100.0	687	2 A46212	MEK kinase - mouse
2	3188.5	92.0	1493	2 T10757	MAP kinase kinase
3	586.5	16.9	651	2 A96591	MAP kinase kinase
4	586.5	16.9	706	2 A48084	STE11 protein kinase
5	574.5	16.6	1478	2 S20117	protein kinase BCK
6	568	16.4	659	1 A39723	protein kinase byr
7	536	15.5	883	2 A96662	hypothetical prote
8	528.5	15.2	738	1 S51380	protein kinase STR
9	525	15.1	1338	2 T30565	MAP kinase kinase
10	519.5	15.0	608	2 G96575	probable MEK kinase
11	499.5	14.4	1116	2 T38073	serine/threonine-p
12	479	13.8	652	2 H86221	hypothetical prote
13	472.5	13.6	582	2 T51625	MAP3K alpha protei
14	462	13.3	608	2 T01833	serine/threonine-s
15	460.5	13.3	1607	2 T03022	MAP kinase kinase
16	448.5	12.9	650	2 JC4673	protein kinase (EC
17	441	12.7	372	2 T52621	mitogen-activated
18	441	12.7	535	2 T51736	mitogen-activated
19	436	12.6	560	2 D85084	probable mitogen-a
20	435.5	12.6	1401	2 T39225	MAP kinase kinase
21	427	12.3	572	2 T01836	serine/threonine-s
22	424.5	12.2	1379	2 JC5778	apoptosis signal-t
23	424	12.2	1579	2 S59801	serine/threonine-S
24	423	12.2	773	2 T01835	protein kinase SSK
25	422	12.2	560	2 T14616	hypothetical prote
26	420	12.1	372	2 T02550	MAP kinase kinase
27	416	12.0	836	2 B96716	probable serine/th
28	411	11.9	1387	2 T16511	hypothetical prote
29	408.5	11.8	1288	2 JE0363	mitogen-activated

30	404.5	11.7	1895	2 T06609	disease resistance
31	395	11.4	471	2 T39232	probable serine th
32	392	11.3	658	2 T39500	serine/threonine-s
33	392	11.3	756	2 T50298	MAP kinase kinase
34	384	11.1	403	2 JC5974	autora-related kin
35	383.5	11.1	525	2 S58682	protein kinase, p2
36	378	10.9	544	2 S40485	serine/threonine-s
37	377.5	10.9	339	2 C86185	hypothetical prote
38	375.5	10.8	544	2 A57597	beta-p21-activated
39	375.5	10.8	545	2 G01773	p21-activated prot
40	374.5	10.8	1230	2 T18256	probable serine/th
41	374.5	10.8	1230	2 T18259	serine/threonine p
42	374	10.8	658	2 G01770	protein kinase Pak
43	373	10.8	1418	2 T15232	hypothetical prote
44	372.5	10.7	939	2 S28394	probable serine/th
45	370.5	10.7	1062	2 S46367	protein kinase CDC

ALIGNMENTS

RESULT 1	
A46212	MEK kinase - mouse
C:Species: Mus musculus (house mouse)	
C:Date: 22-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-May-1999	
C:Accession: A46212	R;Lange-Carter, C.A.; Pleiman, C.M.; Gardner, A.M.; Blumer, K.J.; Johnson, G.L. Science 260, 315-319, 1993
A:Title: A divergence in the MAP kinase regulatory network defined by MEK kinase and Raf.	
A:Reference number: A46212; PMID:93227040; PMID:8385802	
A:Accession: A46212	
A>Status: preliminary; not compared with conceptual translation	
A:Molecule type: nucleic acid	
A:Residues: 1-687 <LAN>	
A:Experimental source: brain	
A:Note: sequence extracted from NCBI backbone (NCBI:129292)	
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo	
C:Keywords: ATP	
F:416-683/Domain: protein kinase homology <KIN>	
F:424-432/Region: protein kinase ATP-binding motif	
Query Match	100.0%; Score 3467; DB 2; Length 687;
Best Local Similarity	Pred. No. 1.3e-133;
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 MTAVAVAVPSKLVMTLNAGSSTFTMRRLMAIDEVEIAEVIQUGVEDTVGDHDSIQ 60
DB	16 MTAVAVAVPSKLVMTLNAGSSTFTMRRLMAIDEVEIAEVIQUGVEDTVGDHDSIQ 75
QY	61 AAAPTSCLENSLEHTVHEKTKGSLATRLASASSDDIDRLAGVSGVPSSTTTQPKR 120
DB	76 AAAPTSCLENSLEHTVHEKTKGSLATRLASASSDDIDRLAGVSGVPSSTTTQPKR 135
QY	121 AVOTKGRPHSQCINSSPLSHAOLMPAPSPASASVSDISKHROQAVPCKIPASAPQ 180
DB	136 AVOTKGRPHSQCINSSPLSHAOLMPAPSPASASVSDISKHROQAVPCKIPASAPQ 195
QY	181 TORKFSLOFORNCSEHRSDQSPVFTQSRPPSSNHRPKSRPPVSGTSKLGATKSS 240
DB	196 TORKFSLOFORNCSEHRSDQSPVFTQSRPPSSNHRPKSRPPVSGTSKLGATKSS 255
QY	241 MTLIDGASRCDDSGGGGNSGNATVPSDETFTVPEDKCRDLVNTLNSIEDLLBAQM 300
DB	256 MTLIDGASRCDDSGGGGNSGNATVPSDETFTVPEDKCRDLVNTLNSIEDLLBAQM 315
QY	301 PSSDTTFVFKSEAVVSPKAEKNDPTKDVVHNQCKEKEEKEEALAIAMASASOD 360
DB	316 PSSDTTFVFKSEAVVSPKAEKNDPTKDVVHNQCKEKEEKEEALAIAMASASOD 375
QY	361 ALPIVQQLVNGEDIIIIQODTPETLPHTAKAKQPYRDABWLKQOIGLGFSSCYQA 420
DB	376 ALPIVQQLVNGEDIIIIQODTPETLPHTAKAKQPYRDABWLKQOIGLGFSSCYQA 435

QY 421 QDVGTGLMAVKQVTVYRNTSSSEQEEVEALREIRRMGHNLNPNIIIRMGATCEKSNYN 480
DB 436 QDVGTGLMAVKQVTVYRNTSSSEQEEVEALREIRRMGHNLNPNIIIRMGATCEKSNYN 495
QY 481 LFIEMWAGSVALLSKYGAFKESVYNTYEQILRGSLYHENOIIHRDVKANLLIDST 540
DB 496 LFIEMWAGSVALLSKYGAFKESVYNTYEQILRGSLYHENOIIHRDVKANLLIDST 555
QY 541 GORLRADFGAARLASKGTGAGEFQGLLGTIAFMAPEVLRGQYGRSCDWSVGCAT 600
DB 556 GORLRADFGAARLASKGTGAGEFQGLLGTIAFMAPEVLRGQYGRSCDWSVGCAT 615
QY 601 EVACAKPMMNAEKSHNLALIFKIASATTAAPSIPSHLSPGLRDVAARCELOPQDRPSPR 660
DB 616 EVACAKPMMNAEKSHNLALIFKIASATTAAPSIPSHLSPGLRDVAARCELOPQDRPSPR 675
QY 661 ELKHVPFRTTW 672
DB 676 ELKHVPFRTTW 687

RESULT 2

A:Accession: T10757
P:Kinase kinase (EC 2.7.1.-) 1 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C:Accession: T10757
R:Xu, S.; Robbins, D.J.; Christerson, L.B.; English, J.M.; Vanderbilt, C.A.; Cobb, M.H.
Proc. Natl. Acad. Sci. U.S.A. 93, 5291-5295, 1996
A:Title: Cloning of rat MEK kinase 1 cDNA reveals an endogenous membrane-associated 195-
A:Reference number: Z17123; MUID:96224276; PMID:8643568
A:Accession: T10757
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1493 <XUS>
A:Cross-references: EMBL:U48596; NID:g1354136; PIDN:AAC52596.1; PID:g1354137
C:Genetics:
A:Gene: MEK1
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; phosphotransferase; protein kinase

Query Match 92.0%; Score 3188.5; DB 2; Length 1493;
Best Local Similarity 91.9%; Pred. No. 5, 2e-122;
Matches 622; Conservative 18; Mismatches 32; Indels 5; Gaps 1;
QY 1 MTAVAVASKVTMTNAGSGTHTFMRRLMAIDVEFIAYIOUGVEDYVGHDSIQ 60
DB 817 MVTVPPLPSKVTMTNAGSGSHFARMRRRLMAIDVEFIAYIOUGSEDTLDGQDSSQ 876
QY 61 AVAPTSCLENSLEHTVREKTKGSLATRLSASSEDISDRLAGVGLPSTTTQOPR 120
DB 877 ALAPRPYPPSSSLERHAHREKTKGSLKATRLSASSEDISDRLAGVGLPSTTTQOPR 936
QY 121 AVQTKRPHSQCINSSPLSHAQMLPAPAPGSSADSV-----DISKRPQAFVBCIK 175
DB 937 TVQTKRPHSQCINSSPLSPQMLPAPAPGSSADSVAVTASDKRPAFVBCIK 996
QY 176 SASPQQRKPSLOFQNCSEHNDSDLSVFTOSRPPSSNTHRPSPRPVSGTSLGD 235
DB 997 SASPQQRKPSLOFQNCSEHNDSEKLSVFTOSRPPSSNTHRAASRPVPSTSKLD 1056
QY 236 ATKSWTLTIGSASRCDSDFFGGGNGNAVIPSEDFVFPVEDKGLDVNTELENSIED 295
DB 1057 ASKNSWTLTIGSASRCDSDFFGGGNGSNAVIPSEDFVFPVEDKGLDVNTELENSIED 1116
QY 296 LEASMPSSDTTVTFKSEVAVLSEKAEENDTYKDVNHNQCKEKEAESEELATAMM 355
DB 1117 LEASMPSSDTTVTFKSEVAVLSEKAEENDTYKDVNHNQCKEKEAESEELATAMM 1176
QY 356 SASDOLPIVPOLOVENGDIIIIQODTETTLPGHTKAKQIPREDAEMLKGOIGGAPS 415
DB 1177 SASDOLPIVPOLOVENGDIIIIQODTETTLPGHTKANEPYREDEMLKGOIGGAPS 1236

QY 416 SCYQADVGTGLMAVKQVTVYRNTSSSEQEEVEALREIRRMGHNLNPNIIIRMGATCE 475
DB 1237 SCYQADVGTGLMAVKQVTVYRNTSSSEQEEVEALREIRRMGHNLNPNIIIRMGATCE 1296
QY 476 KSNYNLFIFEMWAGSVALLSKYGAFKESVYNTYEQILRGSLYHENOIIHRDVKANL 535
DB 1297 KSNYNLFIFEMWAGSVALLSKYGAFKESVYNTYEQILRGSLYHENOIIHRDVKANL 1356
QY 536 LIDSTGQRIRIDFGAARLASKGTGAGEFQGLLGTIAFMAPEVLRGQYGRSCDWSV 595
DB 1357 LIDSTGQRIRIDFGAARLASKGTGAGEFQGLLGTIAFMAPEVLRGQYGRSCDWSV 1416
QY 596 GCALIEMACAKPMMNAEKSHNLALIFKIASATTAAPSIPSHLSPGLRDVAARCELOPQ 655
DB 1417 GCALIEMACAKPMMNAEKSHNLALIFKIASATTAAPSIPSHLSPGLRDVAARCELOPQ 1476
QY 656 RPPSRRLKHVPFRTTW 672
DB 1477 RPPSRRLKHVPFRTTW 1493

RESULT 3

A:Accession: A96591
NPX1-related protein kinase 2 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 17-May-2002
C:Accession: A96591
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chiu, C.W.; Chung, M.K.; Comai, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Hultz, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luoro, J.S.; Maiti, R.; Marzilli, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.; Ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: A96591
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-651 <STO>
A:Cross-references: GB:A805173; NID:99857521; PIDN:AAG00876.1; GSPDB:GN00141
A:Gene: T24C10.7
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 16.9%; Score 586.5; DB 2; Length 651;
Best Local Similarity 42.9%; Pred. No. 4, 1e-17;
Matches 118; Conservative 56; Mismatches 90; Indels 11; Gaps 5;
QY 394 KQYREDAEWLKGQOIGLGAPESSCYQADVGTGLMAVKQVTVYRNTSSQ--EEVEAL 451
DB 63 KQYR---WRGQQLIGRAGFGTYVMGNLDSGELLAVKQVITSNCAKSKETQAHIDL 118
QY 452 REIRRMGHNLNPNIIIRMGATCEKSNYNLFIFEMWAGSVALLSKYGAFKESVYNTY 511
DB 119 REIRRMGHNLNPNIIIRMGATCEKSNYNLFIFEMWAGSVALLSKYGAFKESVYNTY 178
QY 512 QLLRGSLYHENOIIHRDVKANLLIDSTGQRLRADFGAARLASKGTGAGEFQGLLGT 571
DB 179 QLLRGSLYHENOIIHRDVKANLLIDSTGQRLRADFGAARLASKGTGAGEFQGLLGT 235
QY 572 TIAFMAPEVLRGQYGRSCDWSVGCALIEMACAKPMMNAEKSHNLALIFKIASATTA 631
DB 236 TIAFMAPEVLRGQYGRSCDWSVGCALIEMACAKPMMNAEKSHNLALIFKIASATTA 293
QY 632 STPSHLSPGLRDVAARCELOPQDRPSPRELKHP 666
DB 294 STPSHLSPGLRDVAARCELOPQDRPSPRELKHP 328

RESULT 4
A48084
SMP31 protein kinase homolog NP1 - common tobacco
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 19-Dec-1997
C:Accession: A48084
R:Banno, H.; Hirano, K.; Nakamura, T.; Irie, K.; Nomoto, S.; Matsumoto, K.; Machida, Y.
Mol. Cell. Biol. 13, 4745-4752, 1993
A:Title: NP1, a tobacco gene that encodes a protein with a domain homologous to yeast
A:Reference number: A48084; MUID:9330268; PMID:8336712
A:Accession: A48084
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-706 <BAN>
Experimental source: By-2 cells
Description: Sequence extracted from NCBI backbone (NCBI:135697, NCBI:135698)
C:Keywords: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP
F:94-358/Domain: protein kinase ATP-binding motif
F:102-110/Region: protein kinase ATP-binding motif

Query Match: 16.9%; Score 586.5; DB 2; Length 706;
Best Local Similarity 41.7%; Pred. No. 4,4e-17;
Matches 120; Conservative 60; Mismatches 95; Indels 13; Gaps 6;

QY 387 LGHTAKAP--YRED---AEWLKGOQIGLGFSSCYQADYGTGLMAVQYTVVNT 440
DB 74 LPSISKAELPAKARKDTPPIRRKKEGEMIGCGAFGVYGMVNDSEGLAIKEVSIAMNG 133
QY 441 SSEQ--EEVVEALREIRRMGHNLHNPITRLMGATEKSNVNFIFIMAGSVANLLSKY 498
DB 134 ASREKQAVRELEEVNLLKNSHPNIVRYLTABAGSLNLLFVFGSSLSLLGKF 193
QY 499 GAFKESVINTYEQLRGLSYLHENOQIHRDYKANLLIDSTQRLRIADFGAARLASK 558
DB 194 GSPESVIRMYTQQLGLLEYLHKGIMRDIGANILVDNKG-CIKLADFGASKVVEL 252
QY 559 GTCAGFQGLGTIFMAPEVLRGQYGRSCVNVSGCAITIMACAKPPMAEKSNHL 618
DB 253 ATMTG--AKSMKGTPTWMAPEVILQTHGFSADIMVGVCTIIMAGKPPWS--QQYQEV 308
QY 619 ALIFKIASATAPISPSHLSPLRDVAVRCLQPDPRPSRLKHP 666
DB 309 ALFPHIGTKSHPIPEHLSAESKDFLKLQKQEPHLSANLQHP 356

RESULT 5
S20117
protein kinase BCK1 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)
M:Alternate names: protein J0906; protein kinase SLK1; protein kinase SSP1; protein YJL
C:Species: Saccharomyces cerevisiae
C:Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 24-Sep-1999
C:Accession: S20117; S50298; S22285; S19061; JQ1432; S56872; S30794; JQ1118
R:Costigan, C.; Gehring, S.; Snyder, M.
Mol. Cell. Biol. 12, 1162-1178, 1992
A:Title: A synthetic lethal screen identifies SLK1, a novel protein kinase homolog impl
A:Reference number: S20117; MUID:92186847; PMID:1545797
A:Accession: S20117
A:Molecule type: DNA
A:Residues: 1-1478 <COS>
A:Cross-references: EMBL:M84389
Experimental source: Strain S288C
R:Mitsuga, T.; Boles, E.; Schaaf-Geretschlaeger, I.; Schmitt, S.; Zimmermann, F.K.
Yeast 10, 1481-1488, 1994
A:Title: Sequence and function analysis of a 9.74 kb fragment of Saccharomyces cerevisi
A:Reference number: S50295; MUID:9516706; PMID:7811887
A:Accession: S50298
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-1478 <MIO>
A:Cross-references: EMBL:X77923; NID:g640004; PIDN:CAA54896.1; PID:g640009
R:Lee, K.S.; Levin, D.E.

Mol. Cell. Biol. 12, 172-182, 1992
A:Title: Dominant mutations in a gene encoding a putative protein kinase (BCK1) bypass t
A:Reference number: S22285; MUID:92107166; PMID:1729597
A:Accession: S22285
A:Molecule type: DNA
A:Residues: 1-58; 'I', 60-1478 <LEE>
A:Cross-references: EMBL:X60227
A:Experimental source: strain EG123
R:Lee, K.S.; Levin, D.E.
Submitted to the EMBL Data Library, June 1991
A:Description: An extragenic suppressor of mutations in the S. cerevisiae protein kinase
A:Reference number: S19061
A:Accession: S19061
A:Molecule type: DNA
A:Residues: 1-58; 'I', 60-263; 'P', 265-278; 'I', 280-702; 'S', 707-708; 'RP', 714; 'VITMTB', 715-794
A:Cross-references: EMBL:X60227; NID:g3414; PIDN:CAA42786.1; PID:g3415
A:Experimental source: strain EG123
R:Irie, K.; Araki, H.; Oshima, Y.
Gene 108, 139-144, 1991
A:Title: A new protein kinase, SSP1, modulating the SMP3 gene-product involved in plasm
A:Reference number: JQ1432; MUID:92104496; PMID:1840547
A:Accession: JQ1432
A:Molecule type: DNA
A:Residues: 149-1478 <IRI>
A:Cross-references: EMBL:D10389; DDBJ:D90446
R:Mitsuga, T.; Schaaf-Geretschlaeger, I.; Baur, A.; Boles, E.; Chalwatzis, N.; Fournier
submitted to the Protein Sequence Database, September 1995
A:Reference number: S56855
A:Accession: S56855
A:Molecule type: DNA
A:Residues: 1-1478 <MIW>
A:Cross-references: EMBL:249370; NID:g1008269; PIDN:CAA89389.1; PID:g1008270; MIPS:YJL095
R:Chick, M.E.
submitted to the EMBL Data Library, March 1992
A:Reference number: S27437
A:Accession: S30794
A:Molecule type: DNA
A:Residues: 602-959; 'R', 961; 'R', 963-1085; 'V', 1087; 'SLLIANT', 1092-1094; 'RMD', 1101; 'TV', 110
A:Cross-references: EMBL:M88604; NID:g172073; PIDN:AAA21179.1; PID:g172074
C:Genetics:
A:Gene: SGD:BCK1; SLK1; SSP1
A:Cross-references: SGD:S0003631; MIPS:YJL095W
C:Function:
A:Description: phosphotransferase; protein kinase; involved in cell proliferation
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
C:Keywords: ATP; phosphoprotein; phosphotransferase; serine/threonine-specific protein ki
F:1173-1440/Domain: protein kinase homology <KIN>
F:1181-1189/Region: protein kinase ATP-binding motif

Query Match: 16.6%; Score 574.5; DB 2; Length 1478;
Best Local Similarity 24.1%; Pred. No. 2.8e-16;
Matches 211; Conservative 122; Mismatches 270; Indels 271; Gaps 32;

QY 9 FSKLVLMNAGSTHPTRRRLMAIDAEVLAEVQLQVEDVDVQHQSLQAVAPTSGL 68
DB 620 FLKSLFLMTSGKIT-----IKDQKQO-----KKPAPLISE 653
QY 69 ENNSLEHTVAREKTKGLSATRLSASSEDISDLAGVSGVLPSTTTEQPKPA----- 121
DB 654 NNVPKLSVSKSMRSGTSS--LIASD-----VSLVTSSDITSPDEHAGSGRRY 704
QY 122 VOTGRPHSQCINASP-----LSHAQLMPAPASPCSSAPSVPDISKARPQAF 169
DB 705 PGTPTSYDYRVANTPTETELNWNIKEVLSHE-----NADRMVFKTSPKLELNPDKG 758
QY 170 VECUKPSAPQORRKSLOFOR-----NCEHRDPSQSPVFTGSRPP----- 213
DB 759 SKINPTPTTENSKSSFVYLAKDGETEIDPNHRRSPYTKBELAPKAPRPAPNTSPQ 818
QY 214 -----SSNIHRPKPSRPV-----GSTSKLDATKSMTLDLGSASR-- 250
DB 819 RFLSTSKQKPKPIRLVAVASFKIRSKRSKSKPLPQOLLSSPIEASSSSSDSLTSSVTPASTHV 878

QY 251 -CDSPGCG3-----NSGNAVIPSDETVF---TP----- 275
 DB 879 LIPQPKANDVWRRLKTDQDSTSTPSLKMOKVNRSTVSTNSIFSPPLKRG 938
 QY 276 ---VEDKRLDVNTLNSIEPLLEASNP-----SSDTTFKSEVAV--- 315
 DB 939 SKRVVSTSAADIFEE-----NDITPADAPMPFSDSDSDSSDDIWSKKKTPEPN 993
 QY 316 ---LSEKAKENDTYADVHNOKCKEKE-----AEESEALA 350
 DB 994 NENKDEKSDNSSTHDEIFYDSQTDQKERRKTPRSPPVYQNLKFFPRANLDPKPT 1053
 QY 351 IAWMASASODAL-----PIVPOLOVE-----NGEDIIIIQODT 363
 DB 1054 EGIASPTSPKSLDLSLPKNVASSRTEPTSPSRVPDPDSYEFTIQGLNGKNKPLNQAKT 1113
 QY 384 P-----ETLPGH-----TYAKQ---PYRED 400
 DB 1114 PKTKTIRTAHESLARKNSVYLKRONTKMGTRMVEVENHMSINKAKNSKGEYKEF 1173
 QY 401 AEWLKGOQIGLAFSSCYQADWGTGTLMVVKQTVYVRNNSHQEY---VEALREIRN 457
 DB 1174 A-WMKGEMIGKSGFVAVYLCNLTGEMMAVQVE-VPKYSSQNEALISTVEALRSEVST 1231
 QY 458 MGLNHPNIIIRMLGATCEKSNYNLFTEWAGSGSVAMHLSKYGAFKESVIVNTTEQLRGL 517
 DB 1232 LMDLHLNIVQYGFENKNNTYSLFLFYVAGSGSVGLIRMYGRFDEPLIHLITVYLKGL 1291
 QY 518 SYIHENQIIRHDYKANLLIDSTGQRLRIADFGAARLASKGTGAGFQGLIGTAFFMA 577
 DB 1292 AYHSHGIIIRHDKKANLLIDQDG-ICKISDFGISRK--SKDIYSNS-DWTMGATYFWMA 1347
 QY 578 PEULRQGO-YGRSCDVWSVGCATIEWACAKPWNNAEKSHNLIRIKIASATTAAPSPH 636
 DB 1348 PEWVDTKQGISAKVDIWSJGCIWLEMPAGKRPWS---NEVAMFRIKGSKAPPIPD 1404
 QY 637 LSPGL-----RDVAVRCLLEQPDPRPSRELLKHP 666
 DB 1405 TLPLISQIGRNPLDACEINPEKRPANELLISHP 1438

RESULT 6

A39723
 protein kinase byr2 (EC 2.7.1.-) - fission yeast (Schizosaccharomyces pombe)

N.Alternate names: protein kinase ste8
 C.Species: Schizosaccharomyces pombe

C.Date: 14-Feb-1992 #sequence_revision 14-Feb-1992 #text_change 15-Sep-2000
 C.Accession: A39723; S30094; T39860; T40139

R.Wang, Y.; Xu, H.P.; Rieger, M.; Rodgere, L.; Wigler, M.
 Mol. Cell. Biol. 11, 3554-3563, 1991

A>Title: byr2, a Schizosaccharomyces pombe gene encoding a protein kinase capable of pair
 A.Reference number: A39723; MUID:91260705; PMID:2046669

A.Accession: A39723

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-659 <WAN>

A.Cross-references: GB:M74293; NID:q173352; PIDN:AAA35289.1; PID:q173353

R.Styckarsdottir, U.; Egel, R.; Nielsen, O.

Mol. Gen. Genet. 235, 122-130, 1992

A>Title: Functional conservation between Schizosaccharomyces pombe ste8 and Saccharomyces

A.Reference number: S30094; MUID:93062799; PMID:1435723

A.Accession: S30094

A.Molecule type: DNA

A.Residues: 1-659 <STY>

A.Cross-references: EMBL:X68851; NID:gs106; PIDN:CA46731.1; PID:gs107

R.Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.

submitted to the EMBL Data Library, August 1997

A.Reference number: T39860

A.Accession: T39860

A.Status: preliminary; translated from GB/EMBL/DBJ

A.Molecule type: DNA

A.Residues: 1-659 <WOO>

A/Cross-references: EMBL:298270; PIN:CA10981.1; GSPDB:GN00067; SPDB:SPBC1D7.05c
 A/Experimental source: strain 972h-; cosmid CID7
 R/Wood, V.; Rajandream, M.A.; Barrell, B.G.; Skelton, J.; Churcher, C.M.
 submitted to the EMBL Data Library, June 1997
 A/Reference number: 221907
 A/Accession: T40139
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 298-659 <W02>
 A/Cross-references: EMBL:297211; PIDN:CA10150.1; GSPDB:GN00067; SPDB:SPBC2F12.01
 A/Experimental source: strain 972h-; cosmid c2F12
 C/Genetics:
 A/Genes: byr2; ste8
 A/Map position: 2
 C/Superfamily: protein kinase byr2; protein kinase homology; SAM homology
 C/Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
 F.1-56/Domain: SAM homology <SAM>
 F.1-56/Domain: protein kinase homology <KIN>
 F.400-408/Region: protein kinase ATP-binding motif

Query Match 16.4%; Score 568; DB 1; Length 659;

Best local similarity 26.9%; Pred. No. 2,3e-16;

Matches 181; Conservative 112; Mismatches 267; Indels 112; Gaps 24;

QY 46 LGVEDTVDGHQ-----DSIQAVAPTSCLF-----NSLEHTYHREKTKGSLSATRLSAS 95
 DB 46 LGIENTAKKQKQLKQDYLREF-PPCLIRFLACNGQTRAVOSRGDYQCTLIALKKEFL 104
 QY 96 EDISRLAGVSGVLSSTTTEQPKRAVQTKGRPHQCNSSPSLHQAQMFPAAPSCSA 155
 DB 105 EDASKRIVVSSSRKILTEEFKQI-----CFNSSPERDRLLIIVPEKPC--- 152
 QY 156 PSVPDISKH-----RQAFVPCPIKIPASQTORFSLQFORNCSHRDSDQLSP 204
 DB 153 PSFEDLRKWELEIQAOPALSSQSSLSPLSSVLPSTQKQVR-----SNMAP 202
 QY 205 VFTQSRPP--SSNI-----HRPKSRPVGSGTSKLGADATKSSMTLDLSASRCDSP 255
 DB 203 FESYGRPPSELINRSLDFPDHPQPLTEKLTISNRNLISRTSGHNL----- 252
 QY 256 GGGNSGNAVIVSDEIVFPVDEKRLDVNTLNSI-BDL--LEMSWSSDTTVTFKE 312
 DB 253 ---GNFGQELIPRSSRRAPSELVCP--SSLRISVADVNRLLPRIDGPPPLTVSST 306
 QY 313 VAVLSPEKAKENDT-----YKDVNHNQCKEKEKEAE-----EALAIAMMASAS-- 358
 DB 307 QRISRPPSLQKSIITWGVPEPLYQS--NGNEKSKNVFSESAHGNHQLVSFPGSPPT 364
 QY 359 ODALPIVPOLOVNGEDIIIIQODTPETLPGHTAKQPYREDAEWLKGOQIGLAFSSCY 418
 DB 365 EQPSPISP--TSTTSBDTWTLEEDTD-----QSIKWIRGALISGSGFGQY 409
 QY 419 QADQVGTGTLMAVKQVTV--VANTSSQREVEALREIRRMGHNHPNIIIMLGATCK 476
 DB 410 LGNNASSGGLMAVKVITLDVSESSKDRNAKLLDALGELTALLQELSHHTVOYLGSNLS 469
 QY 477 SNVNLPIEMWAGSVAMHLSKYGAFKESVIVNTTEQLRGLSYIHENQIIRHDYKANLL 536
 DB 470 DHNLTFLFVPGSAGLITMGSGPEETIVKPIKOTLGLYLSRGLVHNDIKANLL 529
 QY 537 IDSTGQRLRIADFGAARLA--SKGTAGEFQGLIGTAFFMAPEVLRQGVYGRSCDWS 594
 DB 530 VDNKG-KIKISDFGISKLELNSTSTKTGAPRFGSSFWMAPEVVKQTMTEKTDIWS 588
 QY 595 VGCATIEWACAKPWNNAEKSHNLIRIKIASATTAAPSPISLSTGLRNVAVRCLLEQO 654
 DB 589 LGCLVTEMLTSGPY---PNCDOQALFRIGE-NILPEPNSISSALDFEKTAFIDCN 644
 QY 655 DRPSRELLKHP 666
 DB 645 LRPTASELLSHP 656

RESULT 7

A96662

hypothetical protein F24D7.11 [imported] - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001

C:Accession: A96662

R:Theologos, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, J.; Chinn, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Hansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, K.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
Reference number: A86141; MUID:21016719; PMID:11130712

C:Accession: A96662

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-883 <STO>

A:Cross-references: GB:AEO05173; NID:g6456172; PIDN:AAF09160.1; GSPDB:GN00141

A:Gene: F24D7.11

A:Map position: 1

Query Match 15.5%; Score 536; DB 2; Length 883;
Best Local Similarity 26.1%; Pred. No. 6.1e-15;
Matches 173; Conservative 103; Mismatches 243; Indels 144; Gaps 25;

89 TRLSASSEDISDLGAVGVGLPSTTTEOPKPAVQTKGRPHSGLNS-----SP 137
 57 SRPSSPSSTSTVSRQCSFAERSPAVPLRPVY---RHHVSTDSGMNSQRPGLDAN 112
 138 LSHAQMFAPAPAPCCSAPSVDPDISKRPQAFVPCPKIPASP----- 179
 113 LKSWPLPRK---HGATSPDNTGAKPD-FATASVSSSGVDIPSDLSPLASDCE 167
 180 ---QTKRPSLQQRNCSEHRSDQLSPVTSQRPSPSSNIHRP----- 220
 168 NGNRTPVNISSRQSMNSKMSAEMFKVPNKNRIISASPRRPLGTHVKNLQIPQRLV 227
 221 -----KPSRP-----VPGSTSLG-DATKSSMTLLDLSASRCDDSPFGGSGNSNA 264
 228 LGSAPSLSSPSRSPKRSFTPDQVSHGLISIPYSVDSLGSQC-SFSGSGNSGN 286
 265 VIPSQD-ETVFTVEDKCRDLVNTLNSIEDLLASMPSSDTTVTFKSEVAVLSPE--- 319
 287 SLGDMAVQLFWP-QSRG---SPECSPVSPRMTSPGSSRIQ---SGAVTLHPACG 338
 320 KAENDTYKDVNNQCKEKEKEAEBEELALIMAMASODALPIYQLOVENGEDIIII 379
 339 STTGSPTRRRDDNRQSGHR-----LPLRP-----LII 365
 380 QDQTPETLPHTKA-----KOPYRDA-----EWLKGQIGLGAASSCYAQDVGTF 427
 366 SNTCPSP-PTYSATSPSPSPRAEATVSPSGRWKKGRLGLGSGHGYLLGPNSSGB 424
 428 LMAVKQTVYRNTSSEOEVEALREERIMMGLNHNPIIRMLGATEKSNVLFLEWMA 487
 425 MCMAMKEVTLCSDDPKSRES-AQQLGGEISVLSRLRHQNIYOYGSERVVDKXLYIEVYS 483
 488 GGSVAHLISRYGAFKESVINYTBQLRGLSYHENOIHRDYKGNALLDSTGQRLRIA 547
 484 GGSIVYKLOEYGGFGENAIVNYTQQLISGLAYHAKNTVHRDIKGANILVDPIHG-RVKVA 542
 548 DFGAAAPLAKGAGGAFGQGLGTLAFMAPEVLRGQYGR-SCDVSVGCATIIEMCAK 606
 543 DFGAKKITTQ-SGPLSFK---GSPYMWAPVYIKNSGNSLAVDVISLCTVLEMAATK 597
 607 PPNNAEKGSHNLALIFKIASATTAPSIPLSHSPGLRDAVAVRCLQPODEPPSRHLLKHP 666
 598 PPNNS---QYEGVAPAMFKIGNSKELPDIPLHLSGCKDFYAKCQLQRNANPPTAAQLDDHA 654

RESULT 8

S51380

protein kinase STE11 (EC 2.7.1.-) - yeast (Saccharomyces cerevisiae)

N:Alternate names: protein L8039.10; protein YLR362W

C:Species: Saccharomyces cerevisiae

C:Date: 23-Feb-1995 #sequence_revision 11-Aug-1995 #text_change 21-Jul-2000

C:Accession: S51380; A36456

R:Du, Z.

submitted to the EMBL Data Library, December 1994

A:Description: The sequence of S. cerevisiae cosmid 8039.

A:Reference number: S51377

A:Accession: S51380

A:Molecule type: DNA

A:Residues: 1-738 <DUZ>

A:Cross-references: EMBL:U9103; NID:g609404; PIDN:AAB67571.1; PID:g609414; GSPDB:GN0001;

R:Rhodes, N.; Connell, L.; Ertede, B.

Genes Dev. 4, 1862-1874, 1990

A:Title: STE11 is a protein kinase required for cell-type-specific transcription and sig

A:Reference number: A36456; MUID:91115076; PMID:2276621

A:Accession: A36456

A:Molecule type: DNA

A:Residues: 1-717 <RHO>

A:Cross-references: GB:X53431

C:Gene: SGD:STE11; MIPS:YLR362W

A:Cross-references: SGD:S0004354; MIPS:YLR362W

A:Map position: 12R

C:Superfamily: protein kinase byr2; protein kinase homology; SAM homology

C:Keywords: ATP; phosphotransferase; protein kinase

F:38-104/Domain: SAM homology <SAM>

F:34-733/Domain: protein kinase homology <KIN>

F:442-450/Region: protein kinase ATP-binding motif

Query Match 15.2%; Score 528.5; DB 1; Length 738;
Best Local Similarity 26.5%; Pred. No. 1e-14;
Matches 185; Conservative 104; Mismatches 214; Indels 195; Gaps 28;

26 RMRRLMATADVEIETAEVQLGVEDVDDGHQSLQAV-----APTGLNLSLEHT----Y 77
 172 RLPEHLLATNNGEVTGMQYDVFVLDYTKVNLHLYVELVTTICHADREKKNRLIEV 231
 78 HREKT--GKGLSATR-----LSASEDISDLGAVGVGLPSTTTEOPKPAVQTKGRPH 129
 232 SKQTPSDAISTSKLYRTLSLSQ-----VG-PSSNL-----LAQNGIGH 275
 130 SGLNSPPLSHQMLPAPAPCCSAPSVDPDISKRPQAFVPCPKIPASPOTQRKPSIQ 188
 276 NNAEGLRIDNTE-----KDIRIQIFNQRPSEFISTNLGAGFPHTDMK---R 320
 189 PQNCSE-HRDSQSLSPVTSQRPSPSSNIHRKPRPVPKSGSKGD-ATSSMTLDIG 246
 321 LQKTRSEFRHSRLISA-----QRRPLASBSNNIGDILLKHSNAVDMA 364
 247 SASRCDSFGGSGNSGNAVIPSDEFTVFEVDKCRDLVNTLNSIEDLLASMPSSDTT 306
 365 LLOGLD-----QTRLSKL-----DTT 381
 307 VTFKSEVAVSPKAEENDTYKDVNNQCKEKEKEAEBEELALIMAMASODALPIYF 366
 382 ---KIPKLAKRPBDNDALIS-----NOLBELSVSGEE-----DHDFF----- 417
 367 QLOVENGEEDIIIIQDQTPETLPHTKAKOPYRDAEMLGQOIGLGAFFSCYQAOVGTG 426
 418 ---GDSQDIV---SLP--TKIATP---KMWLKGACIGSGFSQSVYIGMNAHTG 459
 427 TLMAVKQTVYRNT-----SSEOE-----VV 448

Db 460 ELMAVQVEIKNNICVPTDNNKANSDENNEOEQEKIEDVGAIVSHPTKNTNHRKV 519
QY 449 EALREIRRMGHLNHNPIIRMLGATCEKSNYNLFIEIMMAGSVAILSKYGAFKESV 508
Db 520 DALQHMNLKELHNNITTYGASOEGCNLFLEEVCGASVSNLNNYGPFEELITN 579
QY 509 YTEBQIRGLSYLHENQIHRDVKGANLLIDSTGQRLIADFGAARLAKGTGAGEPQO 568
Db 580 FTROILIGVAYLHKNNIHRDIDIGANILIDIKG-CVKITDFGISKPLSKPLNKQNK-RAS 637
QY 569 LIGTIFAMAPEVLRGQOYGRSCDVSVCALIEMACAKPPMNAEKSHNLALIFKIASAT 628
Db 638 LQGSFVMSBEVVKQATTAKADISTGCVVILEMFGKHP---PPSQWALFKIGTNT 694
QY 629 TAPSIPTSHLSPGLRDVAVRCLQLQPODRPPREILKHP 666
Db 695 T-PEIRSMATSEKGNFLRKAFFELDYQRPSEALLQHP 731

RESULT 9

T30565
MAP kinase kinase kinase - Yeast (Kluyveromyces marxianus var. lactis)
C:Species: Kluyveromyces marxianus var. lactis, Candida sphaerica
Accession: T30565
Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
J. Mol. Biol. 288, 337-352, 1999
Kobayashi, J., J. Kirchbach, L. J. Gengenbacher, U. J. Heinisch, J. J.
A. Title: Characterization of KLBCL1, encoding a MAP kinase kinase of Kluyveromyces
A:Reference number: Z20862; MUID:99262846; PMID:10329146
A:Accession: T30565
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1338 <JAC>
A:Cross-references: EMBL:AJ005079; NID:g3021328; PID:CA06336.1; PID:g3021329
C:Genetics:
A:Note: BCK1
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog

Query Match 15.1%; Score 525; DB 2; Length 1338;
Best Local Similarity 27.3%; Pred. No. 2.5e-14;
Matches 182; Conservative 123; Mismatches 267; Indels 95; Gaps 25;
QY 64 PPSCLN---SLEHTVHREKTKGL-----SATRLSASS---EDISD-R 101
Db 676 PAAAKNVSESPLESPPKLDNRGKTIYQKKNRPPPLTERSSRSVSLSGQDINEVK 735
QY 102 LAGVSVGLSSSTTEQPKP---AVQKGRPHSGCLNSSLPSHAQLMFPAPSAFCSSAPSV 158
Db 736 EEPVQSFPASTQVWVPQYKALETL-KPKRS-----SADLSIRPMW 777
QY 159 PDISKRPQAFVPCIKIPASPTQRFKSLQ-----FORNCSEHRSDQLSPV-- 205
Db 778 SLRQFERSNSSLNKLKTLSTSRQLTNRGKPLVTSSTADIPENDISFADAEISDSD 837
QY 206 FTQSRPPSSNIHRPKSRPVPSTSKLDATKSSMTLDLSARCDSDFGGCGNSGN-- 263
Db 838 YGASSDEIITMSDRKSIISNDVPEFSPTED-----TIDLVTGDTTQVSGATEGSDTPK 891
QY 264 --AVIPSDTFTVPVVDKRLDVTNELNSIEDLSAPSSPTTYTPKSEVAVLSPEKA 321
Db 892 KVALRSPSPVYVQNE-KFPDADLD-NPLLEGLTPPSPNADSPSPRPFKSLKTSK 949
QY 322 ENDDTYKDVNNHOK-----CKEKMAEEBEALAIAMASADALPIVQ-LQVEN---- 372
Db 950 EQQPAPLSSRGSSQPLTPVKSILKPKRTKTRIRI-IAQESSEARKNEVQKQKRTTKM 1008
QY 373 GEDIIIIQQDTPELTPLGHTKAKQPYREDAEWLKGQOIGLGFSSCYQAQDVGTGLMAVK 432
Db 1009 GKVVAVITDKRTISIKSRNSREYKEPA-WIKGEIIGKSGFCAVYVLTALNVTGEMLAVK 1067
QY 433 QVTYVANTSSQEQ--EVEALREIRRMGHLNHNPIIRMLGATCEKSNYNLFIEIMAGG 489
Db 1068 QVT-VPEFSSQDESALISWEALKSEVSTLKDLNHNVIQVYLGFEEKNGIYSFLLEVAVG 1126

QY 490 SYAHLISKYGAFAKESVAVINYTEQLRGLSYLHENQIHRDVKGANLLIDSTGQRLIADP 549
Db 1127 SVGSLIRMYGRDDQILRLHTQVLEGLAYLSKGLIHRDMKADNLLDNDV-CRISDF 1185
QY 550 GAARLASKGTGAGEQOGLGTIFAMPEVL-RQOQYRSCDVSVCALIEMACAKPP 608
Db 1186 GISRKSNNTYSN---DMTMRGTVMMAPEWDTAHGSAKVDIWSLGCVLIEMFAGKRP 1242
QY 609 WNAEKSHNLALIFKIASATTAPEISPH-----LSPGLRDVAVRCLQLQPODRPPREILK 664
Db 1243 WS---NFEVVAAMFQIGSKTAPPIPDQTKDVSFAGSGFLDQCETIDPEKFTADSLVG 1299
QY 665 HPEVFTT 671
Db 1300 HPFCKTS 1306

RESULT 10

G96575
Probable MEK kinase MAP3Ka, 84794-81452 (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: G96575
R:Theologis, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hultzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Malt, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzbeyer, S.L.; Schwartz, J.R.; Shim, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Frazer, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A66141; MUID:21016719; PMID:11130712
A:Accession: G96575
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-608 <STO>
A:Cross-references: GB:AB005173; NID:g10645340; PID:AA021460.1; GSPDB:GN00141
C:Genetics:
A:Gene: P22G10.18
A:Map position: 1

Query Match 15.0%; Score 519.5; DB 2; Length 608;
Best Local Similarity 26.7%; Pred. No. 2e-14;
Matches 142; Conservative 86; Mismatches 190; Indels 113; Gaps 14;
QY 190 QNCSSEHRSDQLSPVFTQSRPPSSNIHRPKSRPVPSTSKLDATKSSMTLDLSAS 249
Db 7 RSCSKNKQDNHR--GIISTRDRIKSSAVVDPPLTPTRGGT-----P 46
QY 250 RCDDPFGCGGNGNAVIPEDF-----VFPVVEKCLDVTNELNSIEDLLEAS 299
Db 47 RCSRREF-AGASSAFSGFDSSTEEKGHLPRPLLSFVSIHHDHVGSGTSTSVSVSS 105
QY 300 MESSDT-----TYTFKSEVAVLSPEKAENDDTYKDVNNHOKCKEKMEAEEREA 348
Db 106 SSSADDQSLVARSRGDVKFVVAAPRPERVS----- 139
QY 349 LAIAMASADALPIVQLOVENEDIIIIQDPT-----PETLPGHT 391
Db 140 -----PKATITTRPTSPRHQLSG--VYLSSTGRNDDGRSSSECHPLPRPPTSP 192
QY 392 KAKQPYRED-----AEWLKGOQIGLGFSSCYQAQDVGTGLMAVKQVTVRNTS 441
Db 193 SAVHSGRIIGGYETSPSGFTYKKKPLFSGGTFGGVYIGFENKGMCAIKKVKYISDQ 252
QY 442 SQQEVEALREIRRMGHLNHNPIIRMLGATCEKSNYNLFIEIMAGSVAILSKYGAF 501
Db 253 T-SKRCIKQINBEINLNLQCHPNIVQYGGSLSEBETLSVLEYSGSGIHTLLNDYGSF 311
QY 502 KESVAVINYTEQLRGLSYLHENQIHRDVKGANLLIDSTGQRLIADFGAARLASKGTG 561

```

Db      312 TEVVIQNTVQIILAGLAVLHGRVTVHRDIDIGANILVDPNCE-ITKADFGAKVTAFTST- 369
Qy      562 AGEPQGLCTIAPMAPEVLRGQO-YGRSCDWSVGCATITEMACAKPPMAEKHSNHLAL 620
Db      370 ----MLSEFKSPYMAPEVMSQNGYTHAVDIWSLCTIEMATSKPPMS---QFEGVAA 422
Qy      621 IFKIATATPAPSIPIHSLSPGLRDVAVRCLELOQODRPPRELLKHPFRFTT 671
Db      423 IFKIGNSKOTPEIPDLHLSNDANKFIRLCIQNPVTRPTASOLHEHPRLNT 473

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RESULT 11

```

T38073
Sequence: theonine-protein kinase mbk1 - fission yeast (Schizosaccharomyces pombe)
Accession: T38073
Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
R: Connor, R.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, April 1996
A: Reference number: Z21767
A: Accession: T38073
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-1116 <CON>
A: Cross-references: EMBL:Z70690; PDB:CAA94620.1; GSPDB:GN00066; SPDB:SPAC1F3.02C
A: Experimental source: strain 972h-; contid c1f3
C: Genetics:
A: Gene: pmk1; SPDB:SPAC1F3.02C
A: Map position: 1

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Query Match 14.4%; Score 499.5; DB 2; Length 1116;

Best Local Similarity 24.5%; Pred. No. 2.3e-13;

Matches 174; Conservative 119; Mismatches 293; Indels 123; Gaps 22;

```

Qy      42 EVIQLGVETVDHODSLQAVAPTSCLNSSLBHTVREKTKGL-SATRLSASEDISD 100
Db      429 EITDAGPNLSLGHDP-----NRYGFGSSAPMLAVVPELPSR 467
Qy      101 RLAG-----VSGLPSSITTEQPKPAVOTKGRPHSQCLNSPFLSHAOLMPAPSA 150
Db      468 RFQGFKEIRKAGKEMATKIDATEAGEKKKF-TVCRPHKKVTLKMPLNGSSAPQGPS 526
Qy      151 PCSSASVDPISGRPOAFPCIKIPASPTQKRFSLQFQNCSEHRDSQLSPVFQSR 210
Db      527 NTASAVLTRNFVAHRD---PPPEPTETSLRKNTLT-RRPSLRHARS---SPYIDTGH 578
Qy      211 PPSSNIRHPRKPSRPGVSTKLGADTKSMTLDLGSARCDSPFGGSGNSGNAVIPSDE 270
Db      579 NEASKTSHTSFDPKASKSSNSLKESEVALSEIPEEDAPALDES-DLSDPFWALIQPKOS 637
Qy      271 TVETPVED---KCRLDVNTELNSSLIEDLLEASMPSS-----DTVTVF-----KS 311
Db      638 SSGVPEKNHNHNIQSKSINTEAATDLK-ANELSSPKTPEYCRGDRIISLPSYLRKS 696
Qy      312 EVAVLSPEKAE-----NDPTYKD-----DVFNQCKEKMEA 343
Db      697 KHIRSEPPSSKVINSGNWEVRPSADLDYEDVDRFPFRYDLKYLVDQSMVSSPSKVS 756
Qy      344 EEEBALAIAMAGSODALPIVPOLOVEN-----GEDIIIOODPETLPGH 390
Db      757 RPKMKSVRLARAKASEKKEIRHARANKSGNLRNSTGLMGRSRIYELKPDITTTISGSV 816
Qy      391 TKAKOPYREDDEWLKGOQIGLGAFFSSCYQADVGTGLTMAVKOYTVYRNTSSR---QEE 446
Db      817 VSONATPFK---WMKGELINGTYGKVFLLAMNINTGELIIVAKOYEIPQTINGRHDOQRKD 872
Qy      447 VVALAEETIRMGHINHPNIIIRMLGATCEKSNNTLPIEMAGGSVAHLISKYAFKESVY 506
Db      873 IVDSINAEISMDLHDLNIVQYLFGEKFTDSTIFLEYVSGSISGRCLNNYGFEEQVLV 932
Qy      507 INTTEOLRLGLSYLHENQIIRHVKGANLIDSTGCLRIADFGAARLASKGTGAGEFQ 566

```

```

Db      933 RFVSQVLYGLSYLHSGKIIHRDLKADNLLIDPDGV-CKISDFGISKH--SDNVYNDAN 989
Qy      567 GQLGTTIAPMAPEVLRG--QOYGRSCDWSVGCATITEMACAKPPMAEKHSNHLALIFKI 624
Db      990 LMQGSIIFWMAPEVINHDHOGYSAKADVWSLGCVVIEMLAGRRPWSIDE---AIQAMFKL 1046
Qy      625 ASATATPAPSIPIHSLSPGLRDVAVR-----CLEQODRPPRELLKHPFR 669
Db      1047 GTEKAPPIPSLSELVSOVSPBALQFLNACFTVNADVTRPTAEELNHPMK 1095

```

RESULT 12

```

H86221
hypothetical protein [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H86221
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pedersen, N.A.; Kaul, S.; White, O.; Alonso,
Chen, C.W.; Chung, M.K.; Com, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A: Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.;
C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luores, J.S.; Maitl, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.; Tallon, I.
A: Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A: Reference number: A86141; M0ID:21016719; PMID:11130712
A: Accession: H86221
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-652 <STO>
A: Cross-references: GB:AE005172; NID:G2342692; PDB:AAB70419.1; GSPDB:GN00141
C: Genetics:
A: Map position: 1

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Query Match 13.8%; Score 479; DB 2; Length 652;

Best Local Similarity 37.0%; Pred. No. 9.1e-13;

Matches 112; Conservative 51; Mismatches 90; Indels 50; Gaps 10;

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Qy      388 PGHTKAKOPYREDDEWLKGOQIGLGAFFSSCYQADVGTGLTMAVKOYTVYRNTSSBOEEV 447
Db      57 PANTVMAPE---PISRKQGLIORGAFGYTMGMNIDSGELAVKVLTAANRAS--KEK 111
Qy      448 VVALREIRMGHINHPNII-----RMUGA-----TCEKSN-----YNLFIEWMA 487
Db      112 TQLEEEVKKLKLKSHNIVVSNWYCLLNAGFNTSLCYLSNSVREDDTLNILEFVP 171
Qy      488 GGSVAHLISKYGFKESVYVNTYEQILRGSLYHENOIIRHVKGANLIDSTGQRLRIA 547
Db      172 GGSISLLEKFGFPSPSVARTYRQLLLGLEVLHNAIMHRDIKANILVDNKG-CIKLA 230
Qy      548 DFGAARLASKGAGEFQGLGTTIAPMAPEVL--RGQOYG-----587
Db      231 DFGASQVAVELAMTGT--AKSMKGTIPYMAPEVIIDTGHSPFDLCPILISHKPAIYL 288
Qy      588 RSCDWSVGCATITEMACAKPPMAEKHSNHLALIFKIATATPAPSIPIHSLSPGLRDVAVR 647
Db      289 SSADIVSVGCTVEMTGKAPMS--QOYKEVAIIFIGTKSHPIPDITLSSADKFLK 346
Qy      648 CLE 650
Db      347 CLQ 349

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RESULT 13

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T51625
MAEPK alpha protein kinase (EC 2.7.1.-) [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 08-Sep-2000
C:Accession: T51625
R:Jouanin, S.; Hamal, A.; Lepince, A.S.; Tregear, J.W.; Kreis, M.; Henry, Y.
Gene 229, 171-81, 1999

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